

Sequence listing

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Medeva Europe Limited
- (B) STREET: 10 St James's Street
- (C) CITY: London
- (D) STATE: not applicable
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): SW1A 1EF

(ii) TITLE OF INVENTION: VACCINES CONTAINING ATTENUATED BACTERIA

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0. Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Salmonella typhimurium

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG AAG AAC TGG AAA ACG CTG CTT CTC GGT ATC GCC ATG ATC GCG AAT	48
Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn	
1 5 10 15	
ACC AGT TTC GCT GCC CCC CAG GTA GTC GAT AAA GTC GCA GCC GTC GTC	96
Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val	
20 25 30	
AAT AAT GGC GTC GTG CTG GAA AGC GAC GTT GAT GGC TTA ATG CAA TCA	144
Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser	
35 40 45	

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GTC AAA CTC AAC GCG GGT CAG GCA GGT CAG CAG CTT CCG GAC GAC GCC Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala 50 55 60	192
ACG CTG CGT CAC CAG ATC CTG GAA CGT TTG ATT ATG GAT CAA ATT ATC Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile 65 70 75 80	240
CTG CAG ATG GGT CAG AAG ATG GGG GTG AAG ATC ACG GAT GAG CAG TTG Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu 85 90 95	288
GAT CAG CCA TCA GCC AAC ATC GCC AAA CAA AAC AAT ATG ACG ATG GAT Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp 100 105 110	336
CAG ATG CGC AGC CGT CTG GCT TAC GAT GGG CTG AAC TAT TCA ACC TAC Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr 115 120 125	384
CGT AAC CAG ATT CGT AAA GAG ATG ATT ATC TCT GAA GTG CGC AAC AAT Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn 130 135 140	432
GAG GTT CGT CGC CGT ATC ACC GTT TTG CCG CAA GAA GTT GAC GCG CTG Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu 145 150 155 160	480
GCA AAA CAG ATT GGC ACC CAA AAC GAT GCG AGC ACC GAG CTG AAC CTG Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu 165 170 175	528
AGC CAT ATC CTG ATT GCT CTG CCG GAA AAC CCA ACC TCC GAG CAG GTT Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val 180 185 190	576
AAC GAC GCG CAG CGC CAG GCG GAA AGC ATT GTT GAA GAA GCG CGT AAC Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn 195 200 205	624
GGC GCA GAT TTC GGC AAA CTG GCG ATT ACC TAC TCT GCC GAC CAG CAG Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln 210 215 220	672
GCG CTA AAA GGC GGT CAG ATG GGC TGG GGC CGT ATC CAG GAG CTG CCG Ala Leu Lys Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro 225 230 235 240	720
GGG ATT TTC GCC CAG GCG CTG AGC ACC GCG AAG AAA GGC GAC ATT GTC Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val 245 250 255	768
GGC CCG ATT CGC TCC GGC GTC GGC TTC CAC ATT CTG AAA GTA AAT GAC Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp 260 265 270	816

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CTG CGC GGT CAG AGC CAG AGT ATC TCC GTG ACC GAA GTT CAC GCT CGT 864
 Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val His Ala Arg
 275 280 285

CAC ATT CTG CTT AAG CCG TCG CCG ATC ATG AAC GAT CAG CAG GCG CGC 912
 His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg
 290 295 300

CTG AAG CTG GAA GAA ATC GCG GCT GAC ATT AAG AGT GGT AAA ACC ACC 960
 Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr
 305 310 315 320

TTT GCC GCT GCG GCG AAA GAG TAC TCT CAG GAC CCG GGC TCC GCT AAC 1008
 Phe Ala Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn
 325 330 335

CAG GGC GGT GAT TTG GGT TGG GCT ACG CCA GAT ATT TTC GAC CCG GCG 1056
 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
 340 345 350

TTC CGC GAC GCG CTA ACG AAG CTG CAT AAA GGC CAA ATA AGC GCG CCG 1104
 Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro
 355 360 365

GTA CAC TCC TCT TTC GGC TGG CAT CTG ATC GAA TTG CTG GAT ACG CGT 1152
 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
 370 375 380

AAG GTA GAC AAA ACC GAT GCG GCG CAG AAA GAT CGC GCT TAT CGT ATG 1200
 Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
 385 390 395 400

CTG ATG AAC CGT AAA TTC TCA GAA GAA GCG GCG ACC TGG ATG CAA GAA 1248
 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu
 405 410 415

CAG CGC GCC ACT TAC GTT AAG ATT TTG AGT AAC TAATGA 1287
 Gln Arg Ala Thr Tyr Val Lys Ile Leu Ser Asn
 420 425

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
 1 5 10 15

Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val

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Sein
Cy

	20							25						30	
Asn	Asn	Gly	Val	Val	Leu	Glu	Ser	Asp	Val	Asp	Gly	Leu	Met	Gln	Ser
	35						40						45		
Val	Lys	Leu	Asn	Ala	Gly	Gln	Ala	Gly	Gln	Gln	Leu	Pro	Asp	Asp	Ala
	50					55						60			
Thr	Leu	Arg	His	Gln	Ile	Leu	Glu	Arg	Leu	Ile	Met	Asp	Gln	Ile	Ile
	65				70					75					80
Leu	Gln	Met	Gly	Gln	Lys	Met	Gly	Val	Lys	Ile	Thr	Asp	Glu	Gln	Leu
				85					90						95
Asp	Gln	Pro	Ser	Ala	Asn	Ile	Ala	Lys	Gln	Asn	Asn	Met	Thr	Met	Asp
			100					105						110	
Gln	Met	Arg	Ser	Arg	Leu	Ala	Tyr	Asp	Gly	Leu	Asn	Tyr	Ser	Thr	Tyr
		115					120					125			
Arg	Asn	Gln	Ile	Arg	Lys	Glu	Met	Ile	Ile	Ser	Glu	Val	Arg	Asn	Asn
	130					135						140			
Glu	Val	Arg	Arg	Arg	Ile	Thr	Val	Leu	Pro	Gln	Glu	Val	Asp	Ala	Leu
	145				150					155					160
Ala	Lys	Gln	Ile	Gly	Thr	Gln	Asn	Asp	Ala	Ser	Thr	Glu	Leu	Asn	Leu
				165					170					175	
Ser	His	Ile	Leu	Ile	Ala	Leu	Pro	Glu	Asn	Pro	Thr	Ser	Glu	Gln	Val
			180					185						190	
Asn	Asp	Ala	Gln	Arg	Gln	Ala	Glu	Ser	Ile	Val	Glu	Glu	Ala	Arg	Asn
		195					200					205			
Gly	Ala	Asp	Phe	Gly	Lys	Leu	Ala	Ile	Thr	Tyr	Ser	Ala	Asp	Gln	Gln
	210					215						220			
Ala	Leu	Lys	Gly	Gly	Gln	Met	Gly	Trp	Gly	Arg	Ile	Gln	Glu	Leu	Pro
	225				230				235					240	
Gly	Ile	Phe	Ala	Gln	Ala	Leu	Ser	Thr	Ala	Lys	Lys	Gly	Asp	Ile	Val
			245						250					255	
Gly	Pro	Ile	Arg	Ser	Gly	Val	Gly	Phe	His	Ile	Leu	Lys	Val	Asn	Asp
		260					265						270		
Leu	Arg	Gly	Gln	Ser	Gln	Ser	Ile	Ser	Val	Thr	Glu	Val	His	Ala	Arg
		275					280					285			
His	Ile	Leu	Leu	Lys	Pro	Ser	Pro	Ile	Met	Asn	Asp	Gln	Gln	Ala	Arg
	290					295					300				
Leu	Lys	Leu	Glu	Glu	Ile	Ala	Ala	Asp	Ile	Lys	Ser	Gly	Lys	Thr	Thr
	305				310				315						320

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Sub C1

Phe Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn
325 330 335

Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
340 345 350

Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro
355 360 365

Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
370 375 380

Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
385 390 395 400

Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu
405 410 415

Gln Arg Ala Thr Tyr Val Lys Ile Leu Ser Asn
420 425

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: E.coli

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG AAG AAC TGG AAA ACG CTG CTT CTC GGT ATC GCC ATG ATC GCG AAT 48
Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
430 435 440

ACC AGT TTC GCT GCC CCC CAG GTA GTC GAT AAA GTC GCA GCC GTC GTC 96
Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
445 450 455

AAT AAC GGC GTC GTG CTG GAA AGC GAC GTT GAT GGA TTA ATG CAG TCG 144
Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
460 465 470 475

GTA AAA CTG AAC GCT GCT CAG GCA AGG CAG CAA CTT CCT GAT GAC GCG 192
Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala

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Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg	
700 705 710 715	
CAT ATT CTG CTG AAA CCG TCG CCG ATC ATG ACT GAC GAA CAG GCC CGT	912
His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg	
720 725 730	
GTG AAA CTG GAA CAG ATT GCT GCT GAT ATC GAG AGT GGT AAA ACG ACT	960
Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr	
735 740 745	
TTT GCT GCC GCA ACG AAA GAG TTC TCT CAG GAT CCA GTC TCT GCT AAC	1008
Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn	
750 755 760	
CAG GGC GGC GAT CTC GGC TGG GCT ACA CCA GAT ATT TTC GAT CCG GCC	1056
Gln Gly Glu Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala	
765 770 775	
TTC CGT GAC GCC CTG ACT CGC CTG AAC AAA GGT CAA ATG AGT GCA CCG	1104
Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro	
780 785 790 795	
GTT CAC TCT TCA TTC GGC TGG CAT TTA ATC GAA CTG CTG GAT ACC CGT	1152
Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg	
800 805 810	
AAT GTC GAT AAA ACC GAC GGT GCG CAG AAA GAT CGT GCA TAC CGC ATG	1200
Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met	
815 820 825	
CTG ATG AAC CGT AAG TTC TCG GAA GAA GCA GCA AGC TGG ATG CAG GAA	1248
Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu	
830 835 840	
CAA CGT GCC AGC GCC TAC GTT AAA ATC CTG AGC AAC TAA	1287
Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn	
845 850 855	

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Lys Asn Trp Lys Thr Leu Leu Leu Gly Ile Ala Met Ile Ala Asn
1 5 10 15
Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
20 25 30

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Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
 35 40 45
 Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
 50 55 60
 Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile
 65 70 75 80
 Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu
 85 90 95
 Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp
 100 105 110
 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr
 115 120 125
 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
 130 135 140
 Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu
 145 150 155 160
 Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
 165 170 175
 Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val
 180 185 190
 Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn
 195 200 205
 Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln
 210 215 220
 Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro
 225 230 235 240
 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val
 245 250 255
 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp
 260 265 270
 Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg
 275 280 285
 His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg
 290 295 300
 Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr
 305 310 315 320
 Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn

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Sub C7

325 330 335
Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
340 345 350
Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro
355 360 365
Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
370 375 380
Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
385 390 395 400
Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu
405 410 415
Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn
420 425